

ANS
B2D

Mtb41 (MTCC#2)

SEQUENCE LISTING

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GAGGTTGCTG	GCAATGGATT	TCGGGCTTTT	ACCTCCGGAA	GTGAATTCAA	GCCGAATGTA	60
TTCCGGTCCG	GGGCCGGAGT	CGATGCTAGC	CGCCCGCGGC	GCCTGGGACG	GTGTGGCCGC	120
GGAGTTGACT	TCCGCCGCGG	TCTCGTATGG	ATCGGTGGTG	TCGACGCTGA	TCGTTGAGCC	180
GTGGATGGGG	CCGGCGGCGG	CCCGCATGGC	GGCCGCGGCA	ACGCCGTATG	TGGGGTGGCT	240
GGCCGCCACG	GCGGCGCTGG	CGAAGGAGAC	GGCCACACAG	GCGAGGGCAG	CGGCGGAAGC	300
GTTTGGGACG	GCGTTCGCGA	TGACGGTGCC	ACCATCCCTC	GTCGCGGCCA	ACCGCAGCCG	360
GTTGATGTGCG	CTGGTCGCGG	CGAACATTCT	GGGGCAAAAC	AGTGCAGCGA	TCGCGGCTAC	420
CCAGGCCGAG	TATGCCGAAA	TGTGGGCCC	AGACGCTGCC	GTGATGTACA	GCTATGAGGG	480
GGCATCTGCG	GCCCGCTCGG	CGTTGCCGCC	GTTCACTCCA	CCCGTGCAAG	GCACCGGCC	540
GGCCGGGCC	GCGGCCGAG	CCGCGGGCAG	CCAAGCCGCC	GGTGCAGGGCG	CCGTTGCGGA	600
TGCACAGGGG	ACACTGGCC	AGCTGCC	GGGATCCTG	AGCGACATT	TGTCCGCATT	660
GGCCGCCAAC	GCTGATCCG	TGACATCGG	ACTGTTGGGG	ATCGCGTCGA	CCCTCAACCC	720
GCAAGTCGGA	TCCGCTCAGC	CGATAGTGAT	CCCCACCCCG	ATAGGGGAAT	TGGACGTGAT	780
CGCGCTCTAC	ATTGCATCCA	TCGCGACC	CAGCATTGCG	CTCGCGATCA	CGAACACGGC	840
CAGACCTGG	CACATCGG	TATACGGAA	CGCCGGCGG	CTGGGACCGA	CGCAGGGCA	900
TCCACTGAGT	TCGGCGACCG	ACGAGCCG	GCCGCACTGG	GGCCCCTTCG	GGGGCGCGGC	960
GCCGGTGTCC	GGGGCGTCG	GCCACGCA	ATTAGTCGGA	GCCTGGTCGG	TGCCGCACAG	1020
CTGGACCAAG	GGCCGCCCCG	AGATCCAGC	CGCCGTTCA	GCAACACCCA	CCTTCAGCTC	1080
CAGCGCCGGC	GGCGACCCG	CGGCCCTAA	CGGGATGCCG	GCAGGCC	TCAGCGGGAT	1140
GGCTTTGGCG	AGCCTGGCCG	CACGCGCAC	GACGGGCGGT	GGCCGCACCC	GTAGCGGCAC	1200
CAGCACTGAC	GGCCAAGAGG	ACGGCCCAA	ACCCCCGGTA	TTGTGATTA	GAGAGCAGCC	1260
GCCGCCCGGA	AACCCCCCGC	GGTAAAAGTC	CGCAACCGT	TCGTCGCC	GCGGAAAATG	1320
CCTGGTGAGC	GTGGCTATCC	GACGGGGCGT	TCACACCGCT	TGTAGTAGCG	TACGGCTATG	1380
GACGACGGTG	TCTGGATTCT	CGGGCGCTAT	CAGAGCGATT	TTGCTCGCAA	CCTCAGCAA	1440
G						1441

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Met	Asp	Phe	Gly	Leu	Leu	Pro	Pro	Glu	Val	Asn	Ser	Ser	Arg	Met	Tyr
1										10				15	
Ser	Gly	Pro	Gly	Pro	Glu	Ser	Met	Leu	Ala	Ala	Ala	Ala	Trp	Asp	

20	25	30	
Gly Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val			
35	40	45	
Val Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala			
50	55	60	
Met Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala			
65	70	75	80
Ala Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Ala Glu Ala			
85	90	95	
Phe Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala			
100	105	110	
Asn Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln			
115	120	125	
Asn Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp			
130	135	140	
Ala Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala			
145	150	155	160
Ala Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro			
165	170	175	
Ala Gly Pro Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly			
180	185	190	
Ala Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile			
195	200	205	
Leu Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr			
210	215	220	
Ser Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser			
225	230	235	240
Ala Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile			
245	250	255	
Ala Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile			
260	265	270	
Thr Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly			
275	280	285	
Gly Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu			
290	295	300	
Pro Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala			
305	310	315	320
Gly Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser			
325	330	335	
Trp Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro			
340	345	350	
Thr Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met			
355	360	365	
Pro Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg			
370	375	380	
Gly Thr Thr Gly Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly			
385	390	395	400
Gln Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro			
405	410	415	
Pro Pro Gly Asn Pro Pro Arg			
420			

Mtb40 (HTCC#1)

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

CAGGCATGAG CAGAGCGTTC ATCATCGATC CAACGATCAG TGCCATTGAC GGCTTGTACG	60
ACCTTCTGGG GATTGGAATA CCCAACCAAG GGGGTATCCT TTACTCCTCA CTAGAGTACT	120
TCGAAAAAGC CCTGGAGGAG CTGGCAGCAG CGTTTCCGGG TGATGGCTGG TTAGGTTCGG	180
CCGGGGACAA ATACGCCGGC AAAAACCGCA ACCACGTGAA TTTTTTCCAG GAACTGGCAG	240
ACCTCGATCG TCAGCTCATC AGCCTGATCC ACGACCAGGC CAACCGGGTC CAGACGACCC	300
GCGACATCCT GGAGGGCGCC AAGAAAGGTC TCGAGTTCGT GCGCCCGGTG GCTGTGGACC	360
TGACCTACAT CCCGGTCGTC GGGCACGCC TATCGGCCG CTTCCAGGCG CCGTTTGCG	420
CGGGCGCGAT GGCGTAGTG GGCGGCGCGC TTGCCTACTT GGTCTGTAAA ACGCTGATCA	480
ACCGCACTCA ACTCCTCAAA TTGCTGCCA ATTGGCGGA GTTGGTCGCG GCCGCCATTG	540
CGGACATCAT TTGGATGTC GCGGACATCA TCAAGGGCAC CCTCGGAGAA GTGTGGGAGT	600
TCATCACAAA CGCGCTCAAC GGCCTGAAAG AGCTTTGGGA CAAGCTCACG GGGTGGGTGA	660
CCGGACTGTT CTCTCGAGGG TGGTGAACC TGGAGTCCTT CTTTGCAGGC GTCCCCGGCT	720
TGACCGGCGC GACCAGCGGC TTGTGCAAG TGACTGGCTT GTTGGTGCAG GCCGGTCTGT	780
CCGCATCGTC GGGCTTGGCT CACGCGGATA GCCTGGCGAG CTCAGCCAGC TTGCCCCGCC	840
TGGCCGGCAT TGGGGCGGG TCCGGTTTG GGGGCTTGCC GAGCCTGGCT CAGGTCCATG	900
CCGCCTCAAC TCGGCAGGCG CTACGGCCCC GAGCTGATGG CCCGGTCGGC GCGCTGCG	960
AGCAGGTCGG CGGGCAGTCG CAGCTGGTCT CGCGCAGGG TTCCCAAGGT ATGGGCGGAC	1020
CCGTAGGCAT GGGCGGCATG CACCCCTCTT CGGGGGCGTC GAAAGGGACG ACGACGAAGA	1080
AGTACTCGGA AGGCGCGGGC GCGGGCACTG AAGACGCCGA GCGCGGCCA GTCGAAGCTG	1140
ACCGGGCGG TGGGCAAAAG GTGCTGGTAC GAAACGTCGT CTAACGGCAT GGCGAGCCAA	1200

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Met Ser Arg Ala Phe Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly			
1	5	10	15
Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu			
20	25	30	
Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala			
35	40	45	
Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala			
50	55	60	
Gly Lys Asn Arg Asn Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu			
65	70	75	80
Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln			
85	90	95	
Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val			
100	105	110	

Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
 115 120 125
 Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
 130 135 140
 Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
 145 150 155 160
 Thr Gln Leu Leu Lys Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
 165 170 175
 Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr
 180 185 190
 Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
 195 200 205
 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
 210 215 220
 Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
 225 230 235 240
 Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
 245 250 255
 Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
 260 265 270
 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Ser Gly Phe
 275 280 285
 Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
 290 295 300
 Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
 305 310 315 320
 Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
 325 330 335
 Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
 340 345 350
 Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
 355 360 365
 Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
 370 375 380
 Lys Val Leu Val Arg Asn Val Val
 385 390

Mtb9.9A (MTI-A)

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1742 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*

(xi). SEQUENCE DESCRIPTION: SEQ ID NO: 3.

CCGCTCTCTT TCAACGTCA T AAGTTCGGTG GGCCAGTCGG CCGCGCGTGC ATATGGCACC
AATAACCGCGT GTCCCATGGA TACCCGGACC GCACGACGGT AGAGCGGATC AGCCCCACCCG

60
130

GTGCCGAACA	CTACCGCGTC	CACGCTCAGC	CCTGCCGCGT	TGCCGAAGAT	CGAGCCCAGG	180
TTCTCATGGT	CGTTAACGCC	TTCCAACACT	GCGACGGTGC	GCGCCCCGGC	GACCACCTGA	240
GCAACGCTCG	GCTCCGGCAC	CCGGCGCGCG	GCTGCCAAC	CCCCACGATT	GAGATGGAAG	300
CCGATCACCC	GTGCCATGAC	ATCAGCCGAC	GCTCGATAGT	ACGGCGCGCC	GACACCGGCC	350
AGATCATCCT	TGAGCTCGGC	CAGCCGGCGG	TCGGTGCCGA	ACAGCGCCAG	CGGCGTGAAC	420
CGTGAGGCCA	GCATGCGCTG	CACCACCAAGC	ACACCCCTCGG	CGATCACCAA	CGCTTGGCG	480
GTCGGCAGAT	CGGGACNAVN	GTCGATGCTG	TTCAGGTAC	GGAAATCGTC	GAGCCGTGGG	540
TCGTCGGGAT	CGCAGACGTC	CTGAACATCG	AGGCCGTCGG	GGTGCCTGGG	ACAACGGCCT	600
TCGGTCACGG	GCTTTGCTG	ACCAGAGCCA	GCATCAGATC	GGCGCGCTG	CGCAGGATGT	660
CACGCTCGCT	GCGGTTCAAGC	GTCGCGAGCC	GCTCAGCCAG	CCACTTTC	AGAGAGCCGT	720
TGCTGGGATT	AATTGGGAGA	GGAAAGACAGC	ATGTCGTTTG	TGACCAACACA	GCCGGAAGCC	780
CTGGCAGCTG	CGGCGGCGAA	CCTACAGGGT	ATTGGCACCGA	CAATGAACGC	CCAGAACCGCG	840
GCCCGGGCTG	CTCCAACCAC	CGGAGTAGTG	CCCAGCAGCCG	CCGATGAAGT	ATCAGCGCTG	900
ACCGCGGCTC	AGTTTGCTGC	GCACCGCGAG	ATGTACCAAA	CGGTCA	CCAGGCCGCG	960
GCCATTCAAG	AAATGTTCGT	GAACACCGCTG	GTGGCCAGTT	CTGGCTCATA	CGCGGCCACC	1020
GAGGCGGCCA	ACGCAGCCGC	TGCCGGCTGA	ACGGGCTCGC	ACGAACCTGC	TGAAGGAGAG	1080
GGGGAACATC	CGGAGTTCTC	GGGTCAGGGG	TTGCGCCAGC	GCCCAGCCGA	TTCAGNTATC	1140
GGCGTCATA	ACAGCAGACG	ATCTAGGCAT	TCAGTACTAA	GGAGACAGGC	AACATGGCCT	1200
CACGTTTAT	GACGGATCCG	CATCGATGC	GGGACATGGC	GGGCCGTTTT	GAGGTGACCG	1260
CCCAGACGGT	GGAGGACGAG	GCTCGCCGA	TGTGGGCGTC	CGCGCAAAAC	ATTTCGGGTG	1320
CGGGCTGGAG	TGGCATGGCC	GAGGCACCT	CGCTAGACAC	CATGACCTAG	ATGAATCAGG	1380
CGTTTCGCAA	CATCGTGAAC	ATGCTGCACG	GGGTGCGTGA	CGGGCTGGTT	CGCGACGCCA	1440
ACAANTACGA	ACAGCAAGAG	CAGGCCCTCCC	ACGAGATCCT	GAGCAGNTAG	CGCCGAAAGC	1500
CACAGCTGNG	TACGTTTCT	CACATTAGGA	GAACACCAAT	ATGACGATT	ATTACCAAGTT	1560
CGGGGACGTC	GACGCTCATG	GCGCCATGAT	CCGCGCTCAG	GGGGCGTCG	TTGAGGCGGA	1620
GCATCAGGCC	ATCGTTCGTC	ATGTGTTGGC	CGGGGTGAC	TTTGCGGCG	GCGCCGGTTC	1680
GGTGGCTTGC	CAGGAGTTCA	TTACCCAGTT	GGGCCGTAAC	TTCCACGTGA	TCTACGAGCA	1740
GG						1742

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2836 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE.

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO. 1

GTTGATTCG	TCGCGGCGC	CGCCGAAGAC	CACCAACTCC	GCTGGGTGG	TCGCACAGGC	60
GGTTGCGTCG	GTCAGCTGGC	CGAATCCAA	TGATTGGTGG	CTCNGTGC GG	TTGCTGGGCT	120
CGATTACCCC	CACGGAAAGG	ACGACGATCG	TTCGTTGCT	CGGTCA GTCG	TACTTGGCGA	180
CGGGCATGGC	GCGGTTCTT	ACCTCGATCG	CACAGCAGCT	GACCTTCGGC	CCAGGGGGCA	240
CAACGGCTGG	CTCCGGCGGA	GCCTGGTACC	CAACGCCACA	ATTGCCCGGC	CTGGGTGCAG	300
GCCCCGGCGT	GTCGGCGAGT	TTGGCGGGGG	CGGAGCCGGT	CGGGAGGTTG	TCGGTGCCGC	360
CAAGTTGGC	CGTCGCGGCT	CCGGCCTTCG	CGGAGAAGCC	TGAGGGGGC	ACGCCGATGT	420
CCGTATCGG	CGAAGCGTCC	AGCTGCGGTC	AGGGAGGCCT	GCTTCGAGGC	ATACCGCTGG	480
CGAGAGCGGG	GCCCGTACA	GGCGCCTTCG	CTCACCGATA	CGGGTTCCGC	CACAGCGTGA	540
TTACCCGGTC	TCCGTCGGCG	GGATAGCTT	CGATCCGGTC	TGCGCGGCCG	CCGGAAATGC	600
TGCAGATAGC	GATCGACCGC	GCCGGTCGGT	AAACGCCGCA	CACGGCACTA	TCAATGCGCA	660
CGGCGGGCGT	TGATGCCAAA	TTGACCCGCC	CGACGGGGCT	TTATCTGCGG	CAAGATTTC	720
TCCCCAGCCC	GGTCGGTGGG	CCGATAAAATA	CGCTGGTCAG	CGCGACTCTT	CCGGCTGAAT	780

TCGATGCTCT	GGGCGCCCGC	TCGACGCCGA	GTATCTCGAG	TGGGGCGCAA	ACCCGGTCAA	840
ACGCTGTTAC	TGTGGCGTTA	CCACAGGTGA	ATTTGCGGTG	CCAACTGGTG	AACACTTGCG	900
AACGGGTGGC	ATCGAAATCA	ACTTGGTGC	TTGCAGTGT	CTACTCTCTT	GCAGAGAGCC	960
GTTGCTGGGA	TTAATTGGGA	GAGGAAGACA	GCATGTCGTT	CGTGACCACA	CAGCCGGAAAG	1020
CCCTGGCAGC	TGCGGCGCG	AACCTACAGG	GTATTGGCAC	GACAATGAAC	GCCCAGAACG	1080
CGGCCGCGGC	TGCTCCAACC	ACCGGAGTAG	TGCCCGCAGC	CGCCGATGAA	GTATCAGCGC	1140
TGACCGCGGC	TCAGTTTGCT	GCGCACCGC	AGATGTACCA	AACGGTCAGC	GCCCAGGCCG	1200
CGGCCATTCA	CGAAATGTT	GTGAACACGC	TGGTGGCCAG	TTCTGGCTCA	TACCGGGCCA	1260
CCGAGGGCGC	CAACGCAGCC	GCTGCCGGCT	GAACGGGCTC	GCACGAACCT	GCTGAAGGAG	1320
AGGGGAAACA	TCCGGAGTT	TCGGGTCAAGG	GGTTGCGCCA	GCGCCAGCC	GATTCAAGCTA	1380
TGCGCGTCCA	TAACAGCAGA	CGATCTAGGC	ATTCACTACT	AAGGAGACAG	GCAACATGGC	1440
CTCACGTTT	ATGACGGATC	CGCATGCGAT	GCGGGACATG	GCGGGCGTT	TTGAGGTGCA	1500
CGCCCCAGACG	GTGGAGGAGC	AGGCTCGCCG	GATGTGGGCG	TCCGCGAAA	ACATTTCCGG	1560
TGCGGGCTGG	AGTGGCATGG	CCGAGGGCAGC	CTCGCTAGAC	ACCATGACCT	AGATGAATCA	1620
GGCGTTTCG	AACATCGTGA	ACATGCTGCA	CGGGGTGCGT	GACGGGCTGG	TTCGCGACGC	1680
CAACAACTAC	GAACAGCAAG	AGCAGGCCCTC	CCAGCAGATC	CTGAGCAGCT	AGCGCCGAAA	1740
GCCACAGCTG	CGTACGCTT	CTCACATTAG	GAGAACACCA	ATATGACGAT	TAATTACCAAG	1800
TTCGGGGACG	TCGACGCTCA	TGGGCCATG	ATCCGCGCTC	AGGCGCGTC	GCTTGAGGCG	1860
GAGCATCAGG	CCATCGTTCG	TGATGTGTTG	GCCGCGGGTG	ACTTTGGGG	CGCGCCCGGT	1920
TCGGTGGCTT	GCCAGGAGTT	CATTACCCAG	TTGGGCGTA	ACTTCCAGGT	GATCTACGAG	1980
CAGGCCAACG	CCCACGGGCA	GAAGGGTGCAG	GCTGCCGGCA	ACAACATGGC	GCAAACCGAC	2040
AGCGCCGTCG	GCTCCAGCTG	GGCCTAAAAC	TGAACTTCA	TCGCGGCAGC	ACACCAACCA	2100
GCCGGTGTGC	TGCTGTGTCC	TGCACTAAC	TAGCACTCGA	CCGCTGAGGT	AGCGATGGAT	2160
CAACAGAGTA	CCCGCACCGA	CATCACCGTC	AACGTCGACG	GCTTCTGGAT	GCTTCAGGCG	2220
CTACTGGATA	TCCGCCACGT	TGCGCCTGAG	TTACGTTGCC	GGCGTACGT	CTCCACCGAT	2280
TCCAATGACT	GGCTAAACGA	GCACCCGGGG	ATGGCGGTCA	TGCGCGAGCA	GGGCATTGTC	2340
GTCAACGACG	CGGTCAACGA	ACAGGTCGCT	GCCCCGATGA	AGGTGCTTGC	CGCACCTGAT	2400
CTTGAAGTCG	TGCCCCCTGCT	GTCACGCCGC	AAAGTGCTGT	ACGGGGTCAT	AGACGACGAG	2460
AACCAGCCGC	CGGGTTTCGCG	TGACATCCCT	GACAATGAGT	TCCGGGTGGT	GTTGGCCCGG	2520
CGAGGCCAGC	ACTGGGTGTC	GGCGGTACGG	GTTGGCAATG	ACATCACCGT	CGATGACGTG	2580
ACGGTCTCGG	ATAGCGCCTC	GATCGCCGA	CTGTTAATGG	ACGGTCTGGA	GTCGATTACAC	2640
CACGCCGACC	CAGCCGCGAT	CAACGCGTC	AACTGCCAA	TGGAGGAGAT	CTCGTGCCGA	2700
ATTCCGGCACG	AGGCACGAGG	CGGTGTCGGT	GACGACGGGA	TCGATCACGA	TCATCGACCG	2760
GCCGGGATCC	TTGGCGATCT	CGTTGAGCAC	GACCCGGGCC	CGCGGGAAGC	TCTGCGACAT	2820
CCATGGGTT	TTCCCG					2836

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met	Thr	Ile	Asn	Tyr	Gln	Phe	Gly	Asp	Val	Asp	Ala	His	Gly	Ala	Met
1						5					10				15
Ile	Arg	Ala	Leu	Ala	Gly	Leu	Leu	Glu	Ala	Glu	His	Gln	Ala	Ile	Ile
						20					25				30
Ser	Asp	Val	Leu	Thr	Ala	Ser	Asp	Phe	Trp	Gly	Gly	Ala	Gly	Ser	Ala
						35					40				45

Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
50 55 60
Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
65 70 75 80
Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
85 90

Mtb9.9A (MTI-A) ORF peptides

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Asp Ala His Gly Ala Met Ile Arg Ala Gln Ala Ala Ser Leu Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met Ile Arg Ala Gln Ala Ala Ser Leu Glu Ala Glu His Gln Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val Arg Asp Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala Glu His Gln Ala Ile Val Arg Asp Val Leu Ala Ala Gly Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ile Val Arg Asp Val Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu Phe Ile Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Gly Ser Val Ala Cys Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu
1 5 10 15
Gln Ala

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala Asn Ala His Gly Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ile Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln Thr Asp Ser Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Gly Asn Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
1 5 10 15

Mtb9.8 (MSL)

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGGATTCCGA	TAGCGGTTTC	GGCCCCTCGA	CGGGCGACCA	CGGCGCGCAG	GCCTCCGAAC	60
GGGGGGCCGG	GACCGCTGGGA	TTCGCCCCGA	CCCGAACCAA	AGAACGCCGG	GTCCGGGCGG	120
TCGGGCTGAC	CGCACTGGCC	GGTGTAGAGT	TGGCAACGG	CCCCCGGATG	CCGATGGTGC	180
CGGGGACCTG	GGAGCAGGGC	AGCAACGAGC	CCGAGGCGCC	CGACGGATCG	GGGAGAGGGG	240
GAGGCACGG	CTTACCGCAC	GACAGCAAGT	AACCGAATTG	CGAATCACGT	GGACCCGTAC	300
GGGTCGAAAG	GAGAGATGTT	ATGAGCCTTT	TGGATGCTCA	TATCCCACAG	TTGGTGGCCT	360
CCCAGTCGGC	GTTTGCCGCC	AAGGCAGGGC	TGATGCGGCA	CACGATCGGT	CAGGCCGAGC	420
AGGCAGGGCAG	GTCCGGCTCAG	GCGTTTCACC	AGGGGGAGTC	GTCGGCGGCG	TTTCAGGCCG	480
CCCATGCCCG	GTTTGTGGCG	GCGGCCGCCA	AAGTCAACAC	CTTGTGGAT	GTCGCGCAGG	540
CGAATCTGGG	TGAGGCCGCC	GGTACCTATG	TGGCCGCCGA	TGCTG		585

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
1 5 10 15
Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
20 25 30
Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser

35 40 45
Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys
50 55 60
Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
65 70 75 80
Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ser Thr Tyr Thr Gly
85 90 95
Phe

Mtb9.8 ORF peptides

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Leu Val Ala Ser Gln Ser Ala Phe Ala Ala Lys Ala Gly Leu Met
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Ser Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala Glu Gln Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala Met Ser Ala Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Gln Ala Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly

1

5

10

15

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln Ala Ala His
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Glu Ser Ser Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Ala Arg Phe Val Ala Ala Ala Lys Val Asn Thr Leu Leu Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ala Ala Ala Lys Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val Ala Ala
 1 5 10 15
 Asp Ala

Mtb39A (TbH9)

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GATCGTACCC	GTGCGAGTGC	TCGGGCCGTT	TGAGGATGGA	GTGCACGTGT	CTTCGTGAT	60
GGCATAACCA	GAGATGTTGG	CGGCGGGCGC	TGACACCCCTG	CAGAGCATCG	GTGCTACAC	120
TGTGGCTAGC	AATGCCGCTG	CGGCGGGCCC	GACGACTGGG	GTGGTGCCTT	CCGCTGCCGA	180
TGAGGTGTCG	GCGCTGACTG	CGGCGCACTT	CGCCGCACAT	GCGGCGATGT	ATCAGTCCGT	240
GAGCGCTCGG	GCTGCTGCGA	TTCATGACCA	GTTCGTGGCC	ACCCCTGCCA	GCAGCGCCAG	300
CTCGTATGCG	GCCACTGAAG	TCGCAATGC	GGCGGCGGCC	AGCTAAGCCA	GGAACAGTCG	360
GCACGAGAAA	CCACGAGAAA	TAGGGACACG	TAATGGTGA	TTTCGGGCG	TTACCAACGG	420
AGATCAACTC	CGCGAGGATG	TACGCCGGC	CGGGTTCGGC	CTCGCTGGTG	GCCGCGGCTC	480
AGATGTGGGA	CAGCGTGGCG	AGTACCTGT	TTTCGGCCGC	GTCGGCGTTT	CAGTCGGTGG	540
TCTGGGTCT	GACGGTGGGG	TGGTGGATAG	GTTCGTCCGC	GGGTCTGATG	GTGGCGGCCG	600
CCTCGCGTA	TGTGGCTGTT	ATGAGCGTCA	CCGGGGGGCA	GGCGAGCTG	ACCGCCGCC	660
AGGTCCGGGT	TGCTGCCGCG	GCCTACGAGA	CGGCGTATGG	GCTGACGGTG	CCCCCGCCGG	720
TGATGCCGA	GAACCGTGT	GAACGTATGA	TTCTGATAGC	GACCAACCTC	TTGGGGCAAA	780
ACACCCCGGC	GATCGCGGTC	AACGAGGCCG	AATACGGCGA	GATGTGGGCC	CAAGACGCCG	840
CCGCGATGTT	TGGTACGCGC	CGCGCGACGG	CGACGGCGAC	GGCGACGTTG	CTGCCGTTCG	900
AGGAGGCGCC	GGAGATGACC	AGCGCGGGTG	GGCTCTCTGA	GCAGGCCGCC	GCGGTCGAGG	960
AGGCCTCCGA	CACCGCCGCG	GCGAACAGT	TGATGAACAA	TGTCCCCAG	GCGCTGCAAC	1020
AGCTGGCCCA	GCCCACGCAG	GGCACACCGC	CTTCTTCCAA	GCTGGGTGGC	CTGTGGAAGA	1080
CGGTCTCGCC	GCATCGCTG	CCGATCAGCA	ACATGGTGT	GATGGCAAC	AACCACATGT	1140
CGATGACCAA	CTCGGGTGT	TCGATGACCA	ACACCTTGAG	CTCGATGTTG	AAGGGCTTTG	1200
CTCCGGCGGC	GGCCGCCAG	GCCGTGAAA	CCGGCGCGCA	AAACGGGTC	CGGGCGATGA	1260
GCTCGCTGGG	CAGCTCGCTG	GGTTCTCAG	GTCTGGCGG	TGGGGTGC	GCCAACCTTG	1320
GTCGGGCGGC	CTCGCTCGGT	TCGTTGTCAG	TGCGGCAGGC	CTGGGCCGCG	GCCAACCAGG	1380
CAGTCACCCC	GGCGCGCGG	GCGCTGCCGC	TGACCCAGCCT	GACCAGGCC	GCGGAAAGAG	1440
GGCCCGGGCA	GATGCTGGGC	GGGCTGCCGG	TGGGGCAGAT	GGGCCGCAAG	GCGGGTGGTG	1500
GGCTCAGTGG	TGTGCTGCGT	GTTCCGCCG	GACCCATGAT	GATGCCGCAT	TCTCCGGCGG	1560
CCGGCTAGGA	GAGGGGGCGC	AGACTGTCGT	TATTTGACCA	GTGATCGGC	GTCTCGGTGT	1620
TTCCCGGGCC	GGCTATGACA	ACAGTCAATG	TGCAATGACAA	GTACAGGTA	TTAGGTCCAG	1680
GTTCAACAAAG	GAGACAGGCA	ACATGGCCTC	ACGTTTATG	ACGGATCCGC	ACCGCATGCG	1740
GGACATGGCG	GGCCGTTTG	AGGTGCACCG	CCAGACGGTG	GAGGACGAGG	CTCGCCGGAT	1800
GTGGGCGTCC	GCGAAAACA	TTTCCGGTGC	GGGCTGGAGT	GGCATGGCG	AGGCACCTC	1860
GCTAGACACC	ATGGCCCAGA	TGAATCAGGC	GTTCGCAAC	ATCGTGAACA	TGTCACCGG	1920
GGTGCCTGAC	GGGCTGGTTC	GGCACGCCAA	CAACTACGAG	CAGCAAGAGC	AGGCCTCCCA	1980
GCAGATCCTC	AGCAGCTAAC	GTCAGCCGCT	GCAGCACAA	ACTTTTACAA	GCGAAGGAGA	2040
ACAGGTTCGA	TGACCATCAA	CTATCAATTG	GGGGATGTCG	ACGCTCACGG	CGCCATGATC	2100
CGCGCTCAGG	CCGGGTTGCT	GGAGGCCGAG	CATCAGGCCA	TCATTGCGA	TGTGTTGACC	2160
GGAGTGACT	TTTGGGGCGG	CGCCGGTTCG	GGGGCCTGCC	AGGGGTTCAT	TACCCAGTTG	2220

GGCCGTAACT	TCCAGGTGAT	CTACGAGCAG	GCCAACGCC	ACGGGCAGAA	GGTGCAGGCT	2280
GCCGGCAACA	ACATGGCGCA	AACCGACAGC	GCCGTCGGCT	CCAGCTGGC	CTGACACCAG	2340
GCCAAGGCCA	GGGACGTGGT	GTACGAGTGA	AGTTCCCTCGC	GTGATCCTTC	GGGTGGCAGT	2400
CTAAGTGGTC	AGTGCTGGGG	TGTTGGTGGT	TTGCTGCTTG	GCGGGTTCTT	CGGTGCTGGT	2460
CAGTGCTGCT	CGGGCTCGGG	TGAGGACCTC	GAGGCCAGG	TAGC GCCGTC	CTTCGATCCA	2520
TTCGTCGTGT	TGTTCGGC	GA CGGGCTCC	GACGAGGCGG	ATGATCGAGG	CGCGGT CGGG	2580
GAAGATGCC	ACGACGTCGG	TTCGGCGTCG	TACCTCTCGG	TTGAGGCGTT	CCTGGGGGTT	2640
GTTGGACCA	AGATCTGCTT	GGGAAAGGCC	GTGAACGCCA	GCAGGT CGGT	2700	
GCGGGCGGTG	TCGAGGTGCT	CGGCCACCGC	GGGGAGTTTG	TCGGTCAGAG	CGTCGAGTAC	2760
CCGATCATAT	TGGCAACAA	CTGATT CGGC	GTCGGGCTGG	TCGTAGATGG	AGTGCAGCAG	2820
GGTGCAC	CACGGCCAGG	AGGGCTTCGG	GGTGGCTGCC	ATCAGATTGG	CTGCGTAGTG	2880
GGTTCTGCAG	CGCTGCCAGG	CCGCTGCCGG	CAGGGTGGCG	CCGATCGCGG	CCACCAGGCC	2940
GGCGTGGCG	TCGCTGGTGA	CCAGCGCGAC	CCCAGCAGG	CCGCGGGCGA	CCAGGT CGCG	3000
GAAGAACGCC	AGCCAGCCGG	CCCCGTCC	GGCGGAGGTG	ACCTGGATGC	CCAGGATC	3058

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Met	Val	Asp	Phe	Gly	Ala	Leu	Pro	Pro	Glu	Ile	Asn	Ser	Ala	Arg	Met
1															15

Tyr	Ala	Gly	Pro	Gly	Ser	Ala	Ser	Leu	Val	Ala	Ala	Gln	Met	Trp
														30
20														

Asp	Ser	Val	Ala	Ser	Asp	Leu	Phe	Ser	Ala	Ala	Ser	Ala	Phe	Gln	Ser
															45
35															

Val	Val	Trp	Gly	Leu	Thr	Val	Gly	Ser	Trp	Ile	Gly	Ser	Ser	Ala	Gly
															60
50															

Leu	Met	Val	Ala	Ala	Ala	Ser	Pro	Tyr	Val	Ala	Trp	Met	Ser	Val	Thr
															80
65															

Ala	Gly	Gln	Ala	Glu	Leu	Thr	Ala	Ala	Gln	Val	Arg	Val	Ala	Ala	Ala
															95
85															

Ala	Tyr	Glu	Thr	Ala	Tyr	Gly	Leu	Thr	Val	Pro	Pro	Pro	Val	Ile	Ala
															110
100															

Glu	Asn	Arg	Ala	Glu	Leu	Met	Ile	Leu	Ile	Ala	Thr	Asn	Leu	Leu	Gly
															125
115															

Gln	Asn	Thr	Pro	Ala	Ile	Ala	Val	Asn	Glu	Ala	Glu	Tyr	Gly	Glu	Met
															140
130															

Trp	Ala	Gln	Asp	Ala	Ala	Ala	Met	Phe	Gly	Tyr	Ala	Ala	Ala	Thr	Ala
															160
145															

Thr	Ala	Thr	Ala	Thr	Leu	Leu	Pro	Phe	Glu	Glu	Ala	Pro	Glu	Met	Thr
															175
165															

DRAFT
2/20/2000

Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser
 180 185 190
 Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
 195 200 205
 Gln Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu
 210 215 220
 Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn
 225 230 235 240
 Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val
 245 250 255
 Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala
 260 265 270
 Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala
 275 280 285
 Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly
 290 295 300
 Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val
 305 310 315 320
 Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg
 325 330 335
 Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly
 340 345 350
 Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly
 355 360 365
 Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met
 370 375 380
 Pro His Ser Pro Ala Ala Gly
 385 390

Mtb32A (TbRa35)

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1872 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATACGTTG GTGTAGAAAA ATCCTGCCGC CGGGACCCCTT AAGGCTGGGA CAATTTCTGA

090954 14:11 11/11/95

TAGCTACCCC	GACACAGGAG	GTTACGGGAT	GAGCAATTG	CGCCGCCGCT	CACTCAGGTG	120
GTCATGGTTG	CTGAGCGTGC	TGGCTGCCGT	CGGGCTGGGC	CTGGCCACGG	CGCCGGCCCA	130
GGCGCCCCCG	CCGGCCTTGT	CGCAGGACCG	TTCCCGCGC	TGCCCCTCGA	240	
CCCCTCCGCG	ATGGTCGCC	AAAGTGGCGC	ACAGGTGGTC	AAACATCAACA	CCAAACTGGG	300
CTACAAACAC	GCCGTGGCG	CCGGGACCGG	CATCGTCATC	GATCCCAACG	GTTGTCGTGCT	360
GACCAACAAAC	CACGTGATCG	CGGGCGCCAC	CGACATCAAT	GCGTTAGCG	TGGGCTCCGG	420
CCAAACCTAC	GGCGTCGATG	TGGTCGGGTA	TGACCGCACC	CAGGATGTCG	CGGTGCTGCA	480
GCTGCGCGGT	GCCGGTGGCC	TGCCGTGGC	GGCGATCGGT	GGCGGCGTCG	GGGTTGGTGA	540
GCCCCTCGTC	GCGATGGGCA	ACAGCGGTGG	GCAGGGCGGA	ACGCCCGTG	CGGTGCGCTGG	600
CAGGGTGGTC	GCGCTCGGCC	AAACCGTGA	GGCGTCGGAT	TCGCTGACCG	GTGCCGAAGA	660
GACATTGAAC	GGGTTGATCC	AGTCGATGC	CGCAATCCAG	CCCGGTGATT	GGGGCGGGCC	720
CGTCGTCAAC	GGCCTAGGAC	AGGTGGTCGG	TATGAACACG	GCCGCGTCCG	ATAACTTCCA	780
GCTGTCCAG	GGTGGGCAGG	GATTGCCAT	TCCGATCGGG	CAGGGATGG	CGATCGCGGG	840
CCAAATCCGA	TGGGGTGGGG	GGTCACCCAC	CGTTCATATC	GGGCCTACCG	CCTTCCTCGG	900
CTTGGGTGTT	GTCGACAACA	ACGGCAACGG	CGCACGAGTC	CAACCGTGG	TGGGAAGCGC	960
TCCGGCGGCA	AGTCTCGGCA	TCTCCACCGG	CGACGTGATC	ACCGCGGTG	ACGGCGCTCC	1020
GATCAACTCG	GCCACCGCGA	TGGCGGACGC	GCTTAACGGG	CATCATCCCG	GTGACGTCAT	1080
CTCGGTGAAC	TGGCAAACCA	AGTCGGCGG	CACCGTACA	GGGAACGTGA	CATTGGCCGA	1140
GGGACCCCCG	GCCTGATTTG	TCGCGGATAC	CACCCGCCGG	CCGGCCAATT	GGATTGGCGC	1200
CAGCCGTGAT	TGCGCGTGA	GCCCCCGAGT	TCCGTCTCCC	GTGCGCGTGG	CATTGTGGAA	1260
GCAATGAACG	AGGCAGAACAA	CAGCGTTGAG	CACCCCTCCCG	TGCAGGGCAG	TTACGTCGAA	1320
GGCGGTGTGG	TCGAGCATCC	GGATGCCAAG	GACTTCGGCA	GCGCCGCCGC	CCTGCCCCGC	1380
GATCCGACCT	GGTTTAAGCA	CGCCGTCTTC	TACGAGGTGC	TGGTCCGGC	GTGCTTCGAC	1440
GCCAGCGCGG	ACGGTCCGN	CGATCTCGGT	GGACTCATCG	ATCGCCTCGA	CTACCTGCAG	1500
TGGCTTGGCA	TCGACTGCAT	CTGTTGCCGC	CGTTCCCTACG	ACTCACCCT	GCGGACCGC	1560
GGTTACGACA	TTCGCGACTT	CTACAAGGTG	CTGCCCCGAAT	TCGGCACCGT	CGACGATTTC	1620
GTCGCCCTGG	TCGACACCGC	TCACCGGCCA	GGTATCCGCA	TCATCACCGA	CCTGGTGTGATG	1680
AATCACACCT	CGGAGTCGCA	CCCCTGGTTT	CAGGAGTCCC	GCGCGACCC	AGACGGACCG	1740
TACGGTGACT	ATTACGTGTG	GAGCGACACC	AGCGAGCGCT	ACACCGACGC	CGGGATCATC	1800
TTCGTCGACA	CCGAAGAGTC	GAACCTGGTCA	TTCGATCCTG	TCCGCCGACA	GTTNCTACTG	1860
GCACCGATTCTT						1872

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

Met	Ser	Asn	Ser	Arg	Arg	Ser	Leu	Arg	Trp	Ser	Trp	Leu	Leu	Ser	
1				5			10		15						
Val	Leu	Ala	Ala	Val	Gly	Leu	Gly	Leu	Ala	Thr	Ala	Pro	Ala	Gln	Ala
								20		25					
Ala	Pro	Pro	Ala	Leu	Ser	Gln	Asp	Arg	Phe	Ala	Asp	Phe	Pro	Ala	Leu
							35		40						
Pro	Leu	Asp	Pro	Ser	Ala	Met	Val	Ala	Gln	Val	Ala	Pro	Gln	Val	Val
						50		55							
Asn	Ile	Asn	Thr	Lys	Leu	Gly	Tyr	Asn	Asn	Ala	Val	Gly	Ala	Gly	Thr
						65		70							
Gly	Ile	Val	Ile	Asp	Pro	Asn	Gly	Val	Val	Leu	Thr	Asn	Asn	His	Val
							85		90						
Ile	Ala	Gly	Ala	Thr	Asp	Ile	Asn	Ala	Phe	Ser	Val	Gly	Ser	Gly	Gln
							100		105						
Thr	Tyr	Gly	Val	Asp	Val	Val	Gly	Tyr	Asp	Arg	Thr	Gln	Asp	Val	Ala

115	120	125
Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly		
130	135	140
Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly		
145	150	155
Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu		160
165	170	175
Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr		
180	185	190
Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser		
195	200	205
Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr		
210	215	220
Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala		
225	230	235
Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly		240
245	250	255
Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu		
260	265	270
Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val		
275	280	285
Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile		
290	295	300
Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp		
305	310	315
Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln		320
325	330	335
Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly		
340	345	350
Pro Pro Ala		
355		

Mtb8.4 (DPV)

(2) INFORMATION FOR SEQ ID NO:101

(i) SEQUENCE CHARACTERISTICS

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101.

CGTGGCAATG	TCGTTGACCG	TCGGGGCCGG	GGTCGCCTCC	GCAGATCCCG	TGGACGCGGT	60
CATTAACACC	ACCTGCAATT	ACGGGCAGGT	AGTAGCTGCG	CTCAACCGCA	CGGATCCGGG	120
GGCTGCCGCA	CAGTTCAACG	CCTCACCGGT	GGCGCAGTCC	TATTTGCGCA	ATTCCTCGC	180
CGCACCGCCA	CCTCAGCGCG	CTGCCATGGC	CGCGCAATTG	CAAGCTGTGC	CGGGGGCGGC	240
ACAGTACATC	GGCCTTGTGC	AGTCGGTTGC	CGGCTCCTGC	AACAACATT	AAGCCCCATGC	300
GGGCCCCATC	CCCGCACCCG	GCATCGTCG	CGGGGCTAGG	CCAGATTGCC	CCGCTCCTCA	360
ACGGGCGCGA	TCCCGCGACC	CGGCATCGTC	GCCGGGGCTA	GGCCAGATTG	CCCCGCTCCT	420
CAACGGGCCG	CATCTCGTGC	CGAATTCTG	CAGCCCCGGGG	GATCCACTAG	TTCTAGAGCG	480
GCCGCCACCG	CGGTGGAGCT					500

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Val Ala Met Ser Leu Thr Val Gly Ala Gly Val Ala Ser Ala Asp Pro
1 5 10 15
Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Val Ala
20 25 30
Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Gln Phe Asn Ala Ser
35 40 45
Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro
50 55 60
Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala
65 70 75 80
Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr
85 90 95

Mtb11 (Tb38-1)

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CGGCACGAGA GACCGATGCC GCTACCCTCG CGCAGGAGGC AGGTAATTTC GAGCGGATCT	60
CCGGCGACCT GAAAACCCAG ATCGACCAGG TGGAGTCGAC GGCAGGTTCG TTGCAGGGCC	120
AGTGGCGCGG CGGGCGGGG ACGGCCGCC AGGCCGCGGT GGTGCGCTTC CAAGAACGAG	180
CCAATAAGCA GAAGCAGGAA CTCGACGAGA TCTCGACGAA TATTCGTCAG GCCGGCGTCC	240
AATACTCGAG GGCGACGAG GAGCAGCAGC AGGCCTGTC CTCGCAAATG GGCTTCTGAC	300
CCGCTAATAC GAAAAGAAAC GGAGCAA	327

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile
1 5 10 15
Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly

20	25	30													
Ser	Leu	Gln	Gly	Gln	Trp	Arg	Gly	Ala	Ala	Gly	Thr	Ala	Ala	Gln	Ala
35							40				45				
Ala	Val	Val	Arg	Phe	Gln	Glu	Ala	Ala	Asn	Lys	Gln	Lys	Gln	Glu	Leu
50							55				60				
Asp	Glu	Ile	Ser	Thr	Asn	Ile	Arg	Gln	Ala	Gly	Val	Gln	Tyr	Ser	Arg
65							70				75				80
Ala	Asp	Glu	Glu	Gln	Gln	Gln	Ala	Leu	Ser	Ser	Gln	Met	Gly	Phe	
85							90								95

TbRa3

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTGGCA	CGAGAGGTGA	TCGACATCAT	CGGGACCAGC	CCACATCCT	GGAACAGGC	60
GGCGGCGGAG	GCGGTCCAGC	GGGCGCGGGA	TAGCGTCGAT	GACATCCGCG	TCGCTCGGGT	120
CATTGAGCAG	GACATGGCCG	TGGACAGCGC	CGGCAAGATC	ACCTACCGCA	TCAAGCTCGA	180
AGTGTGTTTC	AAGATGAGGC	CGGCGCAACC	GCGCTAGCAC	GGGCGGGCGA	CCAAGACGCA	240
AAATCGCACG	GTTTGGGTT	GATTGCGCG	ATTTTGTGTC	TGCTCGCCGA	GGCCTACCAG	300
GCGCGGCCCA	GGTCCCGCGT	CTGCCGTATC	CAGGCCTGCA	TCGCGATTCC	GGGGGCCACG	360
CCGGAGTTAA	TGCTTCGCGT	CGACCCGAAC	TGGCGATCC	GCCGGNGAGC	TGATCGATGA	420
CCGTGGCCAG	CCCGTCGATG	CCCGAGTTGC	CCGAGGAAAC	GTGCTGCCAG	GCCGGTAGGA	480
AGCGTCCGTA	GGCGGCGGTG	CTGACCGGCT	CTGCCCTGCGC	CCTCAGTGCG	GCCAGCGAGC	540
GG						542

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Val	Ile	Asp	Ile	Ile	Gly	Thr	Ser	Pro	Thr	Ser	Trp	Glu	Gln	Ala	Ala
1								5			10			15	
Ala	Glu	Ala	Val	Gln	Arg	Ala	Arg	Asp	Ser	Val	Asp	Asp	Ile	Arg	Val
								20			25			30	
Ala	Arg	Val	Ile	Glu	Gln	Asp	Met	Ala	Val	Asp	Ser	Ala	Gly	Lys	Ile
							35			40			45		
Thr	Tyr	Arg	Ile	Lys	Leu	Glu	Val	Ser	Phe	Lys	Met	Arg	Pro	Ala	Gln
							50			55			60		
Pro	Arg														
65															

38kD

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

TGTTCTTCGA CGGCAGGCTG GTGGAGGAAG GGCCCACCGA ACAGCTGTT	60
AGCATCGGGA AACCGCCCGA TACGTGCCG GACTGTCGGG GGACGTCAAG GACGCCAAGC	120
GCGGAAATTG AAGAGCACAG AAAGGTATGG CGTGAAAATT CGTTTGCATA CGCTGTTGGC	180
CGTGTGACCG GCTGCGCCGC TGCTGCTAGC AGCGGCGGGC TGTGGCTCGA AACCAACCGAG	240
CGGTTCGCCT GAAACGGGCG CGGGCGCCGG TACTGTCGCG ACTACCCCCG CGTCGTCGCC	300
GGTGACGTTG GCGGAGACCG GTAGCACGCT GCTCTACCCG CTGTTCAACC TGTGGGGTCC	360
GGCCTTTCAC GAGAGGTATC CGAACGTAC GATCACCGCT CAGGGCACCG GTTCTGGTGC	420
CGGGATCGCG CAGGCCGCCG CGGGGACGGT CAACATTGGG GCCTCCGACG CCTATCTGTC	480
GGAAGGTGAT ATGGCCGCGC ACAAGGGGCT GATGAACATC GCGCTAGCCA TCTCCGCTCA	540
GCAGGTCAAC TACAACCTGC CGGGAGTGAG CGAGCACCTC AAGCTGAACG GAAAAGTCCT	600
GGCGGCCATG TACCAAGGGCA CCATCAAAAC CTGGGACGAC CCGCAGATCG CTGCGCTCAA	660
CCCCGGCGTG AACCTGCCCG GCACCGCGGT AGTTCGCTG CACCGCTCCG ACGGGTCCGG	720
TGACACCTTC TTGTTCACCC AGTACCTGTC CAAGCAAGAT CCCGAGGGCT GGGGCAAGTC	780
GCCCGGCTTC GGCACCAACCG TCGACTTCCC GGCGGTGCCG GGTGCGCTGG GTGAGAACGG	840
CAACGGCGGC ATGGTGACCG GTTGCACCGA GACACGGGC TGCCTGGCCT ATATCGGCAT	900
CAGCTTCCTC GACCAGGCCA GTCAACGGGG ACTCGCGAG GCCAACATAG GCAATAGCTC	960
TGGCAATTTC TTGTTGCCCG ACGCGAAAG CATTCAAGGCC GCGGCGGCTG GCTTCGCATC	1020
GAAAACCCCG GCGAACCAAG CGATTCGAT GATGACGGG CCCGCCCCGG ACGGCTACCC	1080
GATCATCAAC TACGAGTACG CCATCGTAA CAACCGGCAA AAGGACGCCG CCACCGCGCA	1140
GACCTTGCAG GCATTCTGC ACTGGGGCAGT CACCGACGGC AACAAAGGCTT CGTTCCCTCGA	1200
CCAGGTTCAT TTCCAGGCCG TGCCGCCCGC GGTGGTGAAG TTGTCTGACG CGTTGATCGC	1260
GACGATTTCC AGCTAGCTC GTTGAACCAAC ACGGCACAGC AACCTCCGTC GGGCCATCGG	1320
GCTGCTTTGC GGAGCATGCT GGCCCGTGC GGTGAAGTCG GCGCGCTGG CCCGGCCATC	1380
CGGTGGTTGG GTGGGATAGG TGCGGTGATC CCGCTGCTTG CGCTGGTCTT GGTGCTGGTG	1440
GTGCTGGTCA TCGAGGCGAT GGGTGCATC AGGCTCAACG GTTGCATTT CTTCACCGCC	1500
ACCGAATGGA ATCCAGGCAA CACCTACGGC GAAACCGTTG TCACCGACGC GTGCCCATC	1560
CGGTGGCGC CTACTACGGG CGTGTGCCG TGATCGTCGG GACGCTGGCG ACCTCGGCAA	1620
TCGCCCTGAT CATCCGGTG CCGGTCTCTG TAGGAGCGGC GCTGGTGATC GTGGAACGGC	1680
TGCCGAAACG GTTGGCCGAG GCTGTGGGAA TAGTCTGGAA ATTGCTCGCC GGAATCCCCA	1740
GCGTGGTGGT CGGTTGTGG GGGGCAATGA CGTTCGGGCC GTTCATCGCT CATCACATCG	1800
CTCCGGTGT CGCTCACAAAC GCTCCCGATG TGCCGGTGT GAACTACTTG CGCGCGACC	1860
CGGGCAACGG GGAGGGCATG TTGGTGTCCG GTCTGGTGT GGCGGTGATG GTCGTTCCCA	1920
TTATGCCAC CACCACTCAT GACCTGTTCC GGCAGGTGCC GGTGTTGCC CGGGAGGGCG	1980
CGATCGGGAA TTC	1993

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Met Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
 1 5 10 15

Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
 20 25 30

Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
 35 40 45

Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
 50 55 60

Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
 65 70 75 80

Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
 85 90 95

Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
 100 105 110

Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
 115 120 125

Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys
 130 135 140

Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr
 145 150 155 160

Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
 165 170 175

Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
 180 185 190

Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly
 195 200 205

Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
 210 215 220

Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
 225 230 235 240

Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala
 245 250 255

Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn
 260 265 270

Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Gly Phe
 275 280 285

Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro
 290 295 300

Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 305 310 315 320
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
 325 330 335
 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
 340 345 350
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 355 360 365
 Ile Ala Thr Ile Ser Ser
 370

DPEP

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGCATCACC	ATCACCATCA	CATGCATCAG	GTGGACCCCA	ACTTGACACG	TCGCAAGGGA	60
CGATTGGCGG	CACTGGCTAT	CGCGCGATG	GCCAGCGCCA	GCCTGGTGAC	CGTTGCGGTG	120
CCCGCGACCG	CCAACGCCGA	TCCGGAGCCA	GCGCCCCCGG	TACCCACAAAC	GGCCGCCCTCG	180
CCGCGCTCGA	CCGCTGCAGC	GCCACCCCGA	CGGGCGACAC	CTGTTGCCCG	CCCACCCACCG	240
GCCGCCGCCA	ACACGCCGAA	TGCCCAGCCG	GGCGATCCCA	ACGCAGCACC	TCCGCCGGCC	300
GACCCGAACG	CACCGCCGCC	ACCTGTCATT	GCCCCAAACG	CACCCCAACC	TGTCCGGATC	360
GACAACCCGG	TTGGAGGATT	CAGCTTCGCG	CTGCCTGCTG	GCTGGGTGGA	GTCTGACGCC	420
GCCCCACTTCG	ACTACGGTTC	AGCACTCCTC	AGCAAAACCA	CGGGGGACCC	GCCATTTCCC	480
GGACAGCCGC	CGCCGGTGGC	CAATGACACC	CGTATCGTGC	TCGGCCGGCT	AGACCAAAAG	540
CTTTACGCCA	GCGCCGAAGC	CACCGACTCC	AAGGCCGCGG	CCC GGTTGGG	CTCGGACATG	600
GGTGAGTTCT	ATATGCCCTA	CCC GGGCACC	CGGATCAACC	AGGAAACCGT	CTCGCTCGAC	660
GCCAACGGGG	TGTCTGGAAG	CGCGTCGTAT	TACGAAGTCA	AGTTCAGCGA	TCCGAGTAAG	720
CCGAACGGCC	AGATCTGGAC	GGCGTAATC	GGCTCGCCCG	CGGCGAACGC	ACCGGACGCC	780
GGGCCCCCTC	AGCGCTGGTT	TGTGGTATGG	CTCGGGACCG	CCAACAAACCC	GGTGGACAAG	840
GGCGCGGCCA	AGGCCCTGGC	CGAATCGATC	CGGCCTTTGG	TCGCCCCGCC	GCGGGCGCCG	900
GCACCGGCTC	CTGCAGAGCC	CGCTCCGGCG	CGGGCGCCCG	CGGGGAAAGT	CGCTCCTACC	960
CCGACGACAC	CGACACCGCA	CGGGACCTTA	CGGGCCTGA			999

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met	His	His	His	His	Met	His	Gln	Val	Asp	Pro	Asn	Leu	Thr
1					5			10				15	
Arg	Arg	Lys	Gly	Arg	Leu	Ala	Ala	Leu	Ala	Ile	Ala	Ala	Met
					20			25				30	
Ala	Ser	Leu	Val	Thr	Val	Ala	Val	Pro	Ala	Thr	Ala	Asn	Ala
					35			40				45	
Glu	Pro	Ala	Pro	Pro	Val	Pro	Thr	Thr	Ala	Ala	Ser	Pro	Pro
					50			55				60	
Ala	Ala	Ala	Pro	Pro	Ala	Pro	Ala	Thr	Pro	Val	Ala	Pro	Pro
					65			70				75	
Ala	Ala	Ala	Asn	Thr	Pro	Asn	Ala	Gln	Pro	Gly	Asp	Pro	Asn
					85			90				95	
Pro	Pro	Pro	Ala	Asp	Pro	Asn	Ala	Pro	Pro	Pro	Pro	Pro	Pro
					100			105				110	
Asn	Ala	Pro	Gln	Pro	Val	Arg	Ile	Asp	Asn	Pro	Val	Gly	Gly
					115			120				125	
Phe	Ala	Leu	Pro	Ala	Gly	Trp	Val	Glu	Ser	Asp	Ala	Ala	His
					130			135				140	
Tyr	Gly	Ser	Ala	Leu	Leu	Ser	Lys	Thr	Thr	Gly	Asp	Pro	Pro
					145			150				155	
Gly	Gln	Pro	Pro	Pro	Val	Ala	Asn	Asp	Thr	Arg	Ile	Val	Gly
					165			170				175	
Leu	Asp	Gln	Lys	Leu	Tyr	Ala	Ser	Ala	Glu	Ala	Thr	Asp	Ser
					180			185				190	
Ala	Ala	Arg	Leu	Gly	Ser	Asp	Met	Gly	Glu	Phe	Tyr	Met	Pro
					195			200				205	
Gly	Thr	Arg	Ile	Asn	Gln	Glu	Thr	Val	Ser	Leu	Asp	Ala	Asn
					210			215				220	
Ser	Gly	Ser	Ala	Ser	Tyr	Tyr	Glu	Val	Lys	Phe	Ser	Asp	Pro
					225			230				235	
Pro	Asn	Gly	Gln	Ile	Trp	Thr	Gly	Val	Ile	Gly	Ser	Pro	Ala
					245			250				255	
Ala	Pro	Asp	Ala	Gly	Pro	Pro	Gln	Arg	Trp	Phe	Val	Val	Trp
					260			265				270	
Thr	Ala	Asn	Asn	Pro	Val	Asp	Lys	Gly	Ala	Ala	Lys	Ala	Leu
					275			280				285	
Ser	Ile	Arg	Pro	Leu	Val	Ala	Pro	Pro	Ala	Pro	Ala	Pro	Ala
					290			295				300	
Ala	Glu	Pro	Ala	Pro	Ala	Pro	Ala	Pro	Ala	Gly	Glu	Val	Ala
					305			310				315	
Pro	Thr	Thr	Pro	Thr	Pro	Gln	Arg	Thr	Leu	Pro	Ala		
					325			330					

TbH₄

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CGGCACGAGG ATCGGTACCC CGCGGCATCG GCAGCTGCCG ATTGCGCCGGG TTTCCCCCACC

60

CGAGGAAAGC CGCTACCAGA TGGCGCTGCC	GAAGTAGGGC GATCCGTTCG	CGATGCCGGC	120
ATGAAACGGC GGCACTAAAT TAGTGCAGGA ACCTTTCAGT	TTAGCGACGA	TAATGGCTAT	180
AGCACTAAGG AGGATGATCC GATATGACGC AGTCGCAGAC	CGTGACGGTG	GATCAGCAAG	240
AGATTTGAA CAGGGCCAAC GAGGTGGAGG CCCCGATGGC	GGACCCACCG	ACTGATGTCC	300
CCATCACACC GTGCGAACTC ACGGNCGNTA AAAACGCCGC	CCAACAGNTG	GTNTTGTCCG	360
CCGACAACAT GCGGGAAATAC CTGGCGGCCG	GTGCCAAAGA	GCGGCAGCGT	420
CGCTGCCAA CGCGGCCAAG GNGTATGGCG	AGGTTGATGA	GGAGGCTGCG	480
ACAACGACGG CGAAGGAACT GTGCAGGCAG	AATCGGCCGG	GGCCGTCGGA	540
CGGCCGAACT AACCGATAAG CCGAGGGTGG	CCACGGCCGG	TGAACCCAAC	600
TCAAAGAACG CGCAAGGAAG CTCGAAACGG	GCGACCAAGG	CGCATCGCTC	660
GGGATGGGTG GAACACTTNC ACCCTGACGC	TGCAAGGCGA	CG	702

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Gly	Asp	Ser	Phe	Trp	Ala	Ala	Ala	Asp	Gln	Met	Ala	Arg	Gly	Phe	Val
1				5					10					15	
Leu	Gly	Ala	Thr	Ala	Gly	Arg	Thr	Thr	Leu	Thr	Gly	Glu	Gly	Leu	Gln
				20					25					30	
His	Ala	Asp	Gly	His	Ser	Leu	Leu	Leu	Asp	Ala	Thr	Asn	Pro	Ala	Val
				35					40					45	
Val	Ala	Tyr	Asp	Pro	Ala	Phe	Ala	Tyr	Glu	Ile	Gly	Tyr	Ile	Xaa	Glu
				50					55					60	
Ser	Gly	Leu	Ala	Arg	Met	Cys	Gly	Glu	Asn	Pro	Glu	Asn	Ile	Phe	Phe
				65					70					75	
Tyr	Ile	Thr	Val	Tyr	Asn	Glu	Pro	Tyr	Val	Gln	Pro	Pro	Glu	Pro	Glu
				85					90					95	
Asn	Phe	Asp	Pro	Glu	Gly	Val	Leu	Gly	Gly	Ile	Tyr	Arg	Tyr	His	Ala
				100					105					110	
Ala	Thr	Glu	Gln	Arg	Thr	Asn	Lys	Xaa	Gln	Ile	Leu	Ala	Ser	Gly	Val
				115					120					125	
Ala	Met	Pro	Ala	Ala	Leu	Arg	Ala	Ala	Gln	Met	Leu	Ala	Ala	Glu	Trp
				130					135					140	
Asp	Val	Ala	Ala	Asp	Val	Trp	Ser	Val	Thr	Ser	Trp	Gly	Glu	Leu	Asn
				145					150					155	
Arg	Asp	Gly	Val	Val	Ile	Glu	Thr	Glu	Lys	Leu	Arg	His	Pro	Asp	Arg
					165				170					175	
Pro	Ala	Gly	Val	Pro	Tyr	Val	Thr	Arg	Ala	Leu	Glu	Asn	Ala	Arg	Gly
					180				185					190	
Pro	Val	Ile	Ala	Val	Ser	Asp	Trp	Met	Arg	Ala	Val	Pro	Glu	Gln	Ile
				195					200					205	
Arg	Pro	Trp	Val	Pro	Gly	Thr	Tyr	Leu	Thr	Gly	Thr	Asp	Gly	Phe	
				210					215					220	
Gly	Phe	Ser	Asp	Thr	Arg	Pro	Ala	Gly	Arg	Arg	Tyr	Phe	Asn	Thr	Asp
				225					230					235	
Ala	Glu	Ser	Gln	Val	Gly	Arg	Gly	Phe	Gly	Arg	Gly	Trp	Pro	Gly	Arg
					245				250					255	
Arg	Val	Asn	Ile	Asp	Pro	Phe	Gly	Ala	Gly	Arg	Gly	Pro	Pro	Ala	Gln
				260					265					270	
Leu	Pro	Gly	Phe	Asp	Glu	Gly	Gly	Leu	Arg	Pro	Xaa	Lys			

MTbRa12

(2) INFORMATION FOR SEO ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGTATGAAC	ACGGCCGCGT	CCGATAACTT	CCAGCTGTCC	CAGGGTGGGC	AGGGATTTCGC	60
CATTCCGATC	GGGCAGGCGA	TGGCGATCGC	GGGCCAGATC	CGATCGGGTG	GGGGGTCAAC	120
CACCGTTCAT	ATCGGGCCTA	CCGCCTTCCT	CGGCTTGGGT	GTTGTGACAA	ACAACGGCAA	180
CGGCGCACGA	GTCCAACCGG	TGGTCGGGAG	CGCTCCGGCG	GCAAGTCTCG	GCATCTCCAC	240
CGGCGACGTG	ATCACCGCGG	TCGACGGCGC	TCCGATCAAC	TCGGCCACCG	CGATGGGGAA	300
CGCGCTTAAC	GGGCATCATC	CCGGTGTACGT	CATCTCGGTG	AACTGGCAAA	CCAAGTCCCC	360
CGGCACCGCGT	ACAGGGAAACG	TGACATTGGC	CGAGGGACCC	CCGGCCTGAT	TTCGTCGYGG	420
ATACCACCCG	CCGGCCGGCC	AATTGGA				447

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1 5 10 15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
20 25 30
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
35 40 45
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
50 55 60
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
65 70 75 80
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
85 90 95
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
100 105 110
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
115 120 125
Gly Pro Pro Ala
130

```

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

ATGAAGTTGA	AGTTTGCTCG	CCTGAGTACT	GCGATACTGG	GTTGTGCAGC	GGCGCTTGTG	60
TTCCCTGCCT	CGGTTGCCAG	CGCAGATCCA	CTGACCCGC	ATCAGCCGGA	CATGACGAAA	120
GGCTATTGCC	CGGGTGGCCG	ATGGGGTTTT	GGCGACTTGG	CCGTGTGCGA	CGGCGAGAAG	180
TACCCCGACG	GCTCGTTTG	GCACCAAGTGG	ATGCAAACGT	GGTTTACCGG	CCCACAGTTT	240
TACTTCGATT	GTGTCAGCGG	CGGTGAGCCC	CTCCCCGGCC	CGCCGCCACC	GGGTGGTTGC	300
GGTGGGGCAA	TTCCGTCCGA	GCAGCCAAAC	GCTCCCTGA			339

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Met	Lys	Leu	Lys	Phe	Ala	Arg	Leu	Ser	Thr	Ala	Ile	Leu	Gly	Cys	Ala
1				5						10					15
Ala	Ala	Leu	Val	Phe	Pro	Ala	Ser	Val	Ala	Ser	Ala	Asp	Pro	Pro	Asp
				20				25						30	
Pro	His	Gln	Pro	Asp	Met	Thr	Lys	Gly	Tyr	Cys	Pro	Gly	Gly	Arg	Trp
				35				40						45	
Gly	Phe	Gly	Asp	Leu	Ala	Val	Cys	Asp	Gly	Glu	Lys	Tyr	Pro	Asp	Gly
	50				55				60						
Ser	Phe	Trp	His	Gln	Trp	Met	Gln	Thr	Trp	Phe	Thr	Gly	Pro	Gln	Phe
65					70				75					80	
Tyr	Phe	Asp	Cys	Val	Ser	Gly	Gly	Glu	Pro	Leu	Pro	Gly	Pro	Pro	Pro
					85				90					95	
Pro	Gly	Gly	Cys	Gly	Gly	Ala	Ile	Pro	Ser	Glu	Gln	Pro	Asn	Ala	Pro
					100				105					110	

ESAT-6

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

ATGACAGAGC AGCAGTGGAA TTTCGCGGGT ATCGAGGCCG CGGCAAGCGC AATCCAGGGA	60
AATGTCACGT CCATTCATTC CCTCCTTGAC GAGGGGAAGC AGTCCCTGAC CAAGCTCGCA	120
GCGGCCTGGG GCGGTAGCGG TTCGGAAGCG TACC	154

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser			
1	5	10	15
Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly			
20	25	30	
Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser			
35	40	45	
Glu Ala Tyr			
50			

02668672 101000